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## SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG  
 <120> Method for the recombinant expression of an N-terminal fragment of hepatocyte growth factor  
 <130> 22388 WO  
 <150> EP 04004951.2  
 <151> 2004-03-03  
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 act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa aaa 96  
 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys  
 20 25 30  
 gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa gga 144  
 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
 35 40 45  
 ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa caa 192  
 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
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 tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa gaa 240  
 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu  
 65 70 75 80  
 ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga aac 288  
 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn  
 85 90 95

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tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc act	336
Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr	
100 105 110	
aag agt ggc atc aaa tgt cag ccc tgg agt tcc atg ata cca cac gaa	384
Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu	
115 120 125	
cac agc ttt ttg cct tcg agc tat cgg ggt aaa gac cta cag gaa aac	432
His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn	
130 135 140	
tac tgt cga aat cct cga ggg gaa gaa ggg gga ccc tgg tgt ttc aca	480
Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr	
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agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag tgt tca	528
Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser	
165 170 175	
gaa gtt gaa tgc atg acc tgc aat ggg gag agt tat cga ggt ctc atg	576
Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met	
180 185 190	
gat cat aca gaa tca ggc aag att tgt cag cgc tgg gat cat cag aca	624
Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr	
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cca cac cgg cac aaa ttc ttg cct gaa aga tat ccc gac aag ggc ttt	672
Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe	
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Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys	
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tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att aaa aca	768
Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr	
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Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr	
260 265 270	
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Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr	
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att tgg aat gga att cca tgt cag cgt tgg gat tct cag tat cct cac	912
Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His	
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Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu	
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aat tac tgc cga aat cca gat ggg tct gaa tca ccc tgg tgt ttt acc 1008  
Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr  
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act gat cca aac atc cga gtt ggc tac tgc tcc caa att cca aac tgt 1056  
Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys  
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gat atg tca cat gga caa gat tgt tat cgt ggg aat ggc aaa aat tat 1104  
Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr  
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atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca atg tgg 1152  
Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp  
370 375 380

gac aag aac atg gaa gac tta cat cgt cat atc ttc tgg gaa cca gat 1200  
Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp  
385 390 395 400

gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat gat gct 1248  
Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala  
405 410 415

cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg gat tat 1296  
His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr  
420 425 430

tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca ata gtc aat 1344  
Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn  
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Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
35 40 45

Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
50 55 60

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Cys 65	Leu	Trp	Phe	Pro	Phe 70	Asn	Ser	Met	Ser	Ser 75	Gly	Val	Lys	Lys	Glu 80
Phe	Gly	His	Glu	Phe 85	Asp	Leu	Tyr	Glu	Asn 90	Lys	Asp	Tyr	Ile	Arg 95	Asn
Cys	Ile	Ile	Gly 100	Lys	Gly	Arg	Ser	Tyr 105	Lys	Gly	Thr	Val	Ser 110	Ile	Thr
Lys	Ser	Gly 115	Ile	Lys	Cys	Gln	Pro 120	Trp	Ser	Ser	Met	Ile 125	Pro	His	Glu
His 130	Ser	Phe	Leu	Pro	Ser	Ser 135	Tyr	Arg	Gly	Lys	Asp 140	Leu	Gln	Glu	Asn
Tyr 145	Cys	Arg	Asn	Pro	Arg 150	Gly	Glu	Glu	Gly	Gly 155	Pro	Trp	Cys	Phe	Thr 160
Ser	Asn	Pro	Glu	Val 165	Arg	Tyr	Glu	Val	Cys 170	Asp	Ile	Pro	Gln	Cys 175	Ser
Glu	Val	Glu	Cys 180	Met	Thr	Cys	Asn	Gly 185	Glu	Ser	Tyr	Arg	Gly 190	Leu	Met
Asp	His	Thr 195	Glu	Ser	Gly	Lys	Ile 200	Cys	Gln	Arg	Trp	Asp 205	His	Gln	Thr
Pro 210	His	Arg	His	Lys	Phe	Leu 215	Pro	Glu	Arg	Tyr	Pro 220	Asp	Lys	Gly	Phe
Asp 225	Asp	Asn	Tyr	Cys	Arg 230	Asn	Pro	Asp	Gly	Gln 235	Pro	Arg	Pro	Trp	Cys 240
Tyr	Thr	Leu	Asp	Pro 245	His	Thr	Arg	Trp	Glu 250	Tyr	Cys	Ala	Ile	Lys 255	Thr
Cys	Ala	Asp	Asn 260	Thr	Met	Asn	Asp	Thr 265	Asp	Val	Pro	Leu	Glu 270	Thr	Thr
Glu	Cys	Ile	Gln	Gly	Gln	Gly	Glu 280	Gly	Tyr	Arg	Gly	Thr 285	Val	Asn	Thr

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Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His  
 290 295 300

Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu  
 305 310 315 320

Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr  
 325 330 335

Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys  
 340 345 350

Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr  
 355 360 365

Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp  
 370 375 380

Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp  
 385 390 395 400

Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala  
 405 410 415

His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr  
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Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn  
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Leu Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg  
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Lys	Thr	Thr	Leu	Ile	Lys	Ile	Asp	Pro	Ala	Leu	Lys	Ile	Lys	Thr	Lys	
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aaa	gtg	aat	act	gca	gac	caa	tgt	gct	aat	aga	tgt	act	agg	aat	aaa	144
Lys	Val	Asn	Thr	Ala	Asp	Gln	Cys	Ala	Asn	Arg	Cys	Thr	Arg	Asn	Lys	
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Gly	Leu	Pro	Phe	Thr	Cys	Lys	Ala	Phe	Val	Phe	Asp	Lys	Ala	Arg	Lys	
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Gln	Cys	Leu	Trp	Phe	Pro	Phe	Asn	Ser	Met	Ser	Ser	Gly	Val	Lys	Lys	
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gaa	ttt	ggc	cat	gaa	ttt	gac	ctc	tat	gaa	aac	aaa	gac	tac	att	aga	288
Glu	Phe	Gly	His	Glu	Phe	Asp	Leu	Tyr	Glu	Asn	Lys	Asp	Tyr	Ile	Arg	
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Asn	Cys	Ile	Ile	Gly	Lys	Gly	Arg	Ser	Tyr	Lys	Gly	Thr	Val	Ser	Ile	
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Thr	Lys	Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	Ser	Ser	Met	Ile	Pro	His	
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aac	tac	tgt	cga	aat	cct	cga	ggg	gaa	gaa	ggg	gga	ccc	tgg	tgt	ttc	480
Asn	Tyr	Cys	Arg	Asn	Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	Phe	
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Thr	Ser	Asn	Pro	Glu	Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	Cys	
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tca	gaa	gtt	gaa	tgc	atg	acc	tgc	aat	ggg	gag	agt	tat	cga	ggc	ctc	576
Ser	Glu	Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	
			180					185					190			
atg	gat	cat	aca	gaa	tca	ggc	aag	att	tgt	cag	cgc	tgg	gat	cat	cag	624
Met	Asp	His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	
		195					200					205				

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aca	cca	cac	cgg	cac	aaa	ttc	ttg	cct	gaa	aga	tat	ccc	gac	aag	ggc	672
Thr	Pro	His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	
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Phe	Asp	Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	
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tgc	tat	act	ctt	gac	cct	cac	acc	cgc	tgg	gag	tac	tgt	gca	att	aaa	768
Cys	Tyr	Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	
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aca	tgc	gct	gac	aat	act	atg	aat	gac	act	gat	gtt	cct	ttg	gaa	aca	816
Thr	Cys	Ala	Asp	Asn	Thr	Met	Asn	Asp	Thr	Asp	Val	Pro	Leu	Glu	Thr	
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Thr	Glu	Cys	Ile	Gln	Gly	Gln	Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Val	Asn	
		275					280					285				
acc	att	tgg	aat	gga	att	cca	tgt	cag	cgt	tgg	gat	tct	cag	tat	cct	912
Thr	Ile	Trp	Asn	Gly	Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	Pro	
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Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ser	Pro	Trp	Cys	Phe	
			325					330						335		
acc	act	gat	cca	aac	atc	cga	gtt	ggc	tac	tgc	tcc	caa	att	cca	aac	1056
Thr	Thr	Asp	Pro	Asn	Ile	Arg	Val	Gly	Tyr	Cys	Ser	Gln	Ile	Pro	Asn	
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tgt	gat	atg	tca	cat	gga	caa	gat	tgt	tat	cgt	ggg	aat	ggc	aaa	aat	1104
Cys	Asp	Met	Ser	His	Gly	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Lys	Asn	
		355					360					365				
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Tyr	Met	Gly	Asn	Leu	Ser	Gln	Thr	Arg	Ser	Gly	Leu	Thr	Cys	Ser	Met	
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tgg	gac	aag	aac	atg	gaa	gac	tta	cat	cgt	cat	atc	ttc	tgg	gaa	cca	1200
Trp	Asp	Lys	Asn	Met	Glu	Asp	Leu	His	Arg	His	Ile	Phe	Trp	Glu	Pro	
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Asp	Ala	Ser	Lys	Leu	Asn	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asp	Asp	
				405					410					415		
gct	cat	gga	ccc	tgg	tgc	tac	acg	gga	aat	cca	ctc	att	cct	tgg	gat	1296
Ala	His	Gly	Pro	Trp	Cys	Tyr	Thr	Gly	Asn	Pro	Leu	Ile	Pro	Trp	Asp	
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tat tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca atc gtt	1344
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taa tag	1350
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Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys
50 55 60

Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys
65 70 75 80

Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg
85 90 95

Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile
100 105 110

Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His
115 120 125

Glu His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu
130 135 140



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Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe  
 145 150 155 160

Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys  
 165 170 175

Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu  
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Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln  
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Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly  
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Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp  
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Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys  
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Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr  
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Thr Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn  
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Thr Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro  
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His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg  
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Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe  
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Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn  
 340 345 350

Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn  
 355 360 365

Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met  
 370 375 380

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Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro  
385 390 395 400

Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp  
405 410 415

Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp  
420 425 430

Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
435 440 445